

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

1-24. cancelled

25. (currently amended) A method for identifying a genetic region associated with responsiveness to an agent, the method comprising:
- (a) providing a plurality of single-nucleotide polymorphisms and a plurality of haplotypes for one or more regions of a chromosome;
  - (b) identifying the number of single-nucleotide polymorphisms of said plurality in at least weak linkage disequilibrium with each other on said chromosomal regions;
  - (c) comparing the number of single-nucleotide polymorphisms in linkage disequilibrium to the number of haplotypes in said chromosomal regions; and
  - (d) selecting a correlation test, wherein a single nucleotide-based correlation test is selected if the number of single-nucleotide polymorphisms in linkage disequilibrium is smaller than the number of haplotypes and a haplotype-based correlation test is selected if the number of single-nucleotide polymorphisms in linkage disequilibrium is greater than the number of haplotypes, thereby identifying a genetic region associated with responsiveness to an agent.
26. (currently amended) The method of claim 25, wherein the ~~haplotype-based~~ correlation test is a regression test.
27. (currently amended) The method of claim 25, wherein the ~~haplotype-based~~ correlation test is ANOVA test.